Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data
(M13, Long Gel, 55C, T=6%)
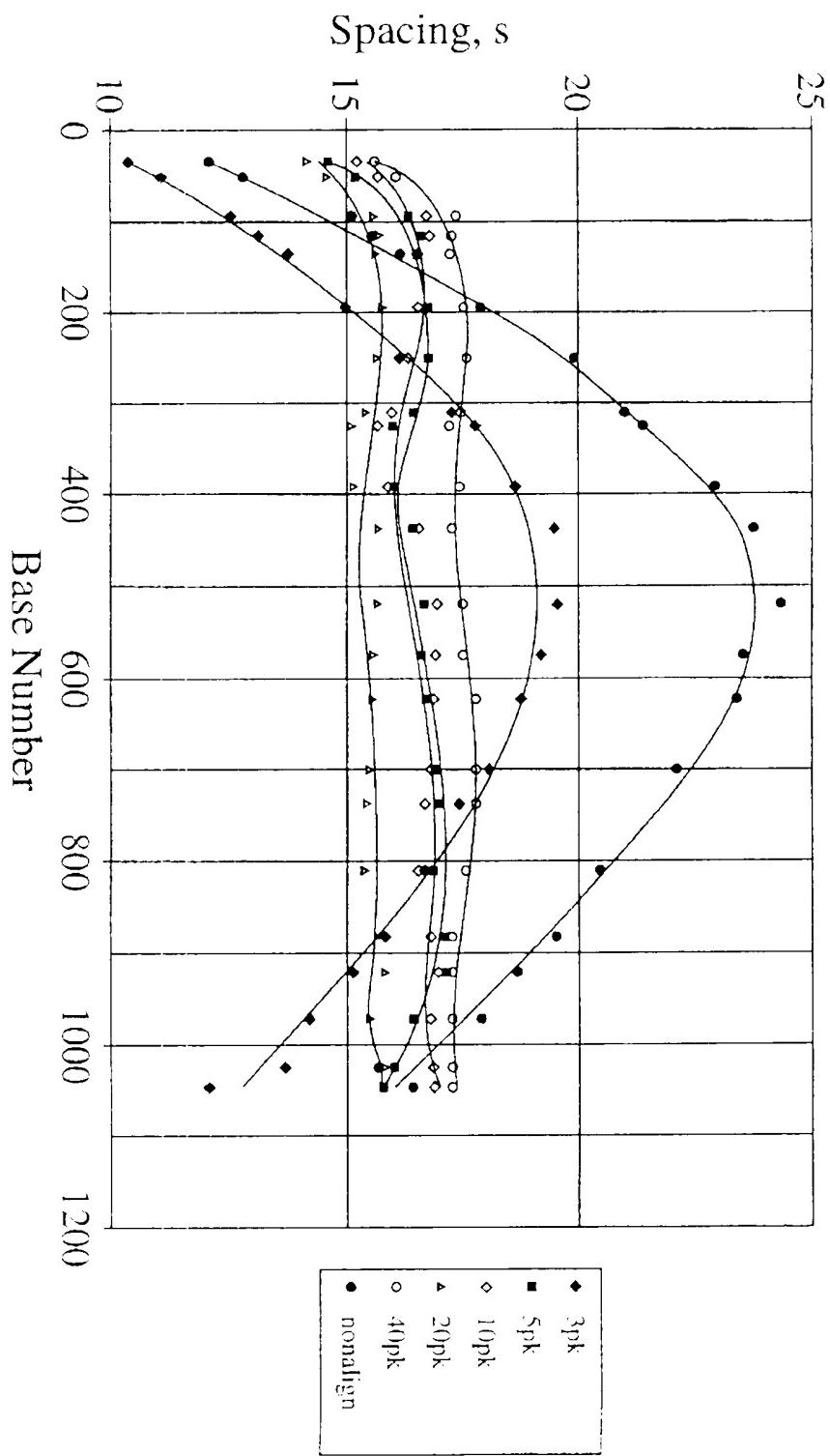
FIG. 2
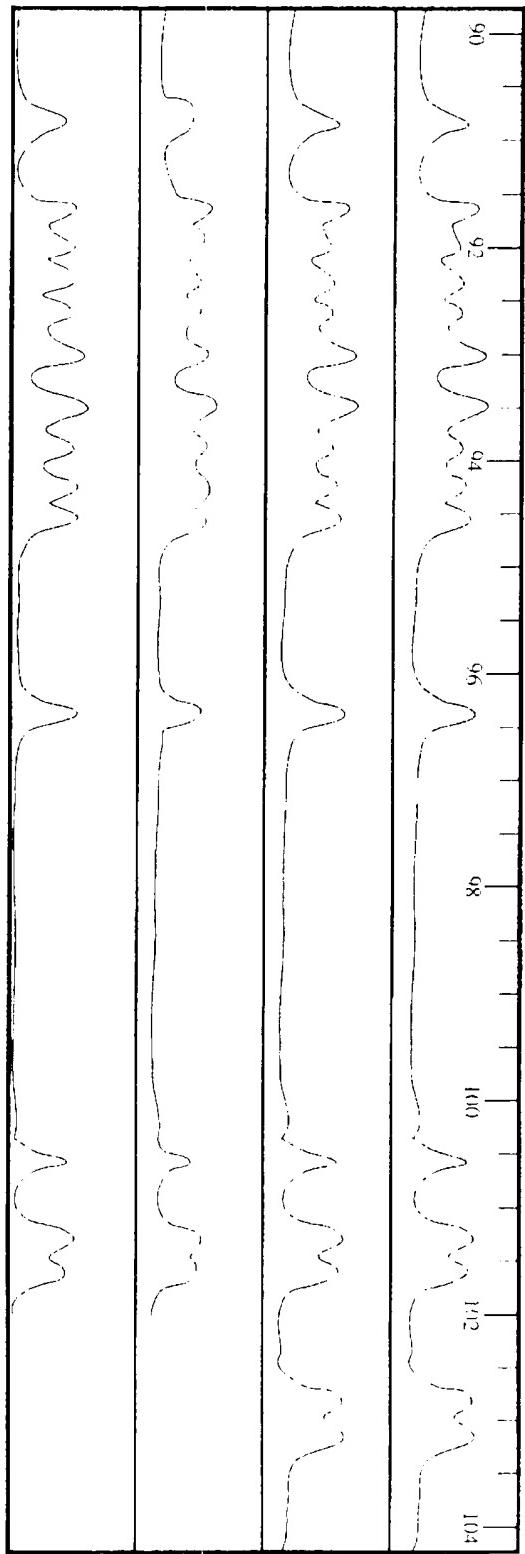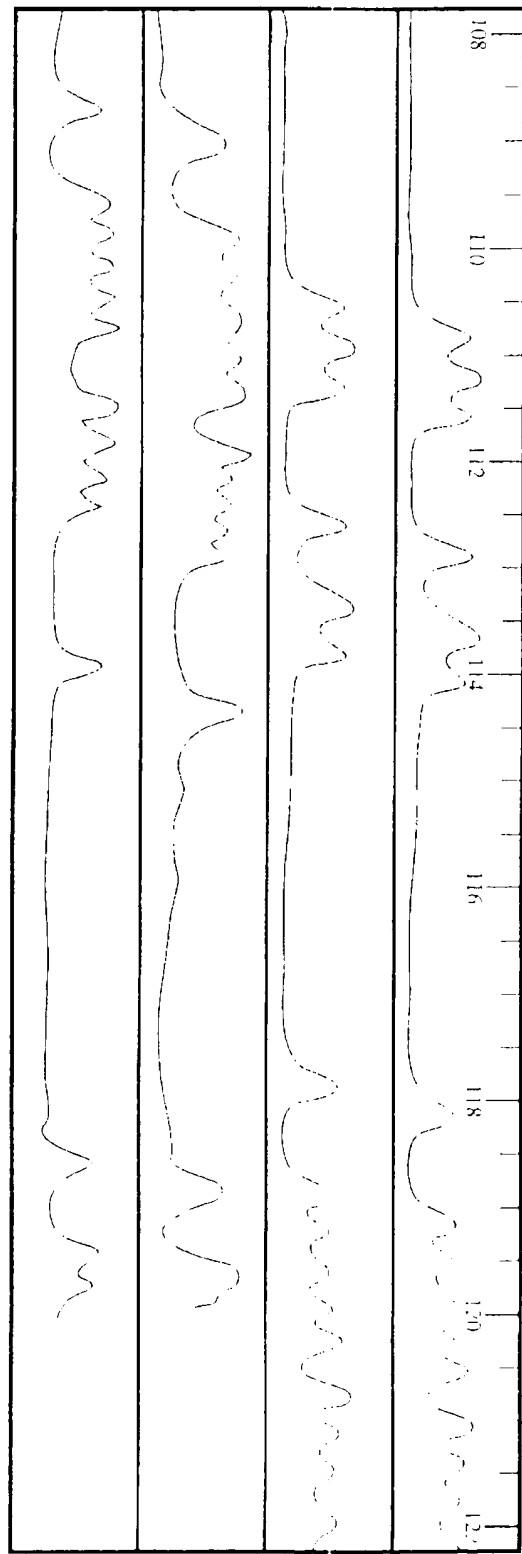
**FIG. 4**

# HIV-1 TruGene Kit (version 0.80)

RT-PCR amplicon (1.3 kbp)

gag polyprotein

pol polyprotein

prot

RT

integrase

vif

env polyprotein

complete nucleotide sequence

2034

2212
2253
2549
2550
3221
3639
4222
5096
5096

distance (kbp)

0   1   2   3   4   5   6   7
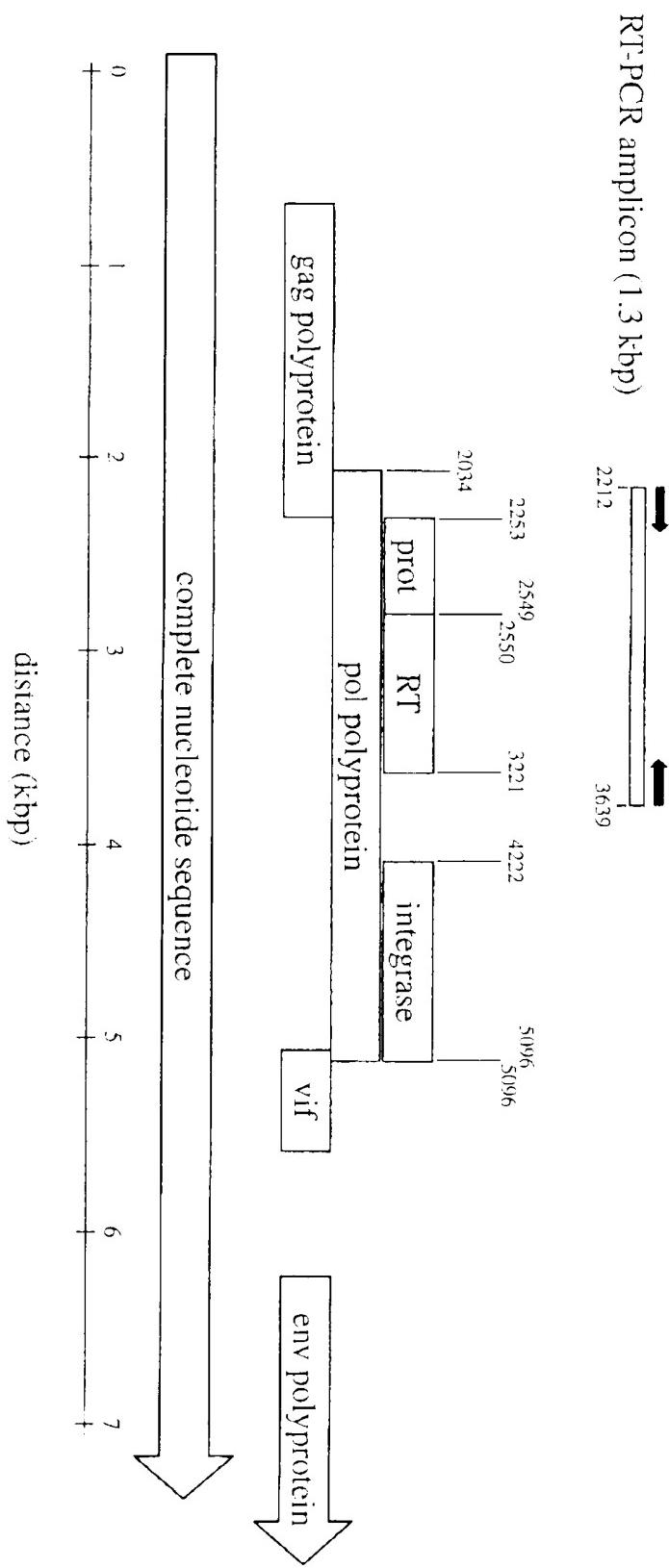
FIG. 6

Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc
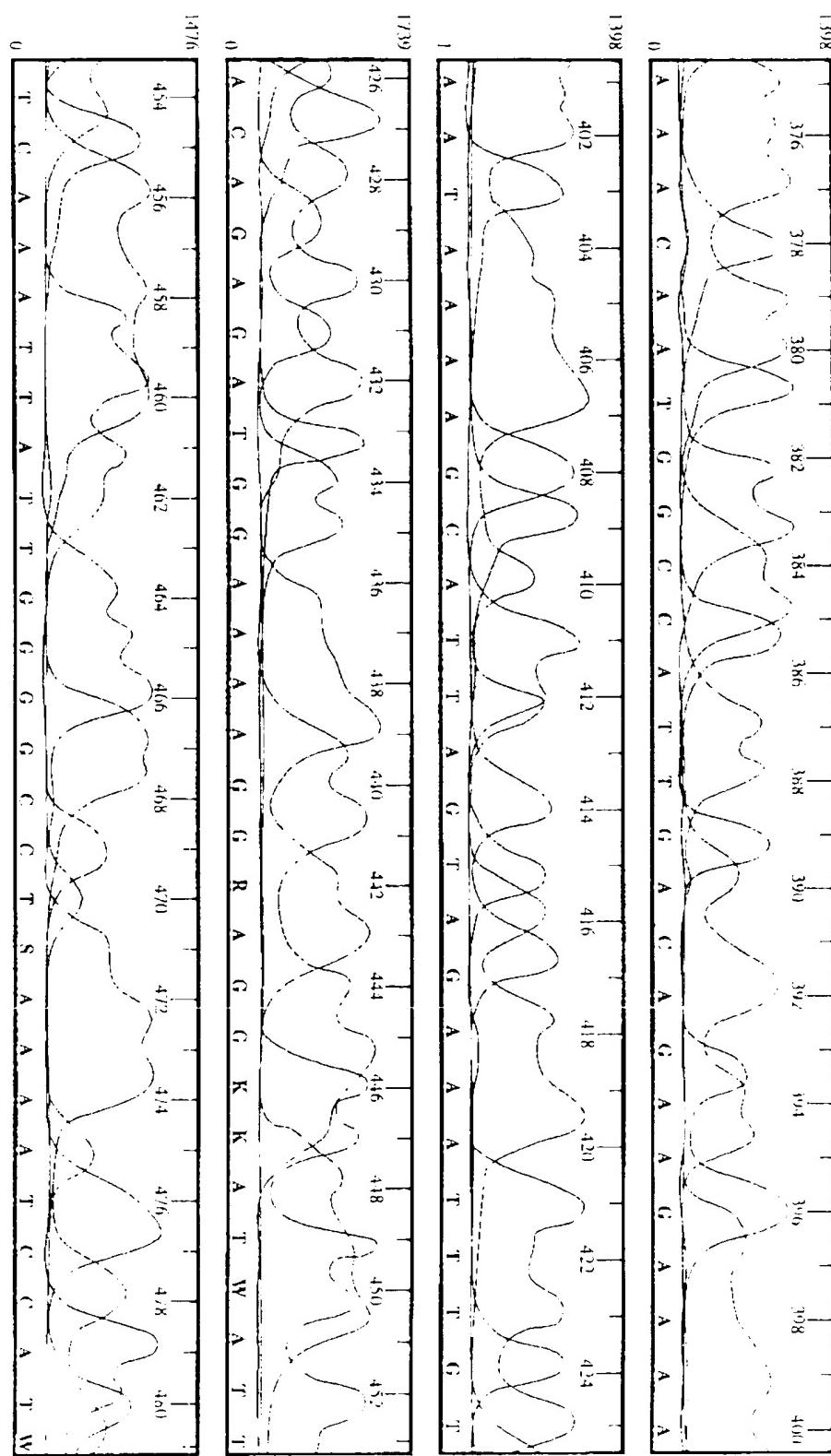
FIG. 7

Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

Block #1: intervening block
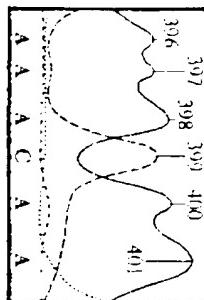
Block #2: alignment block
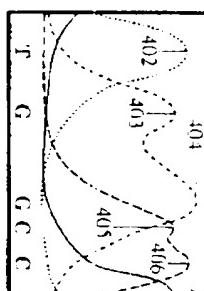
Block #3: intervening block

Block #4: alignment block
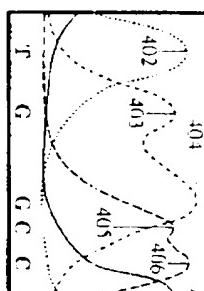
Block #5: intervening block
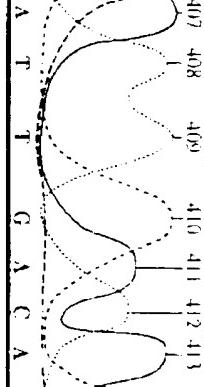
Block #6: alignment block
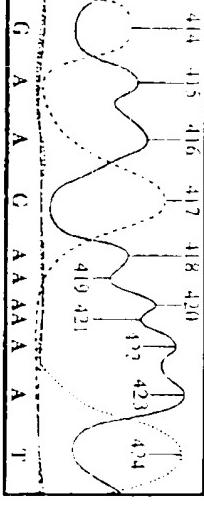
Block #7: intervening block

Block #8: alignment block

Block #9: intervening block
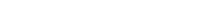
**FIG. 8**

Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc
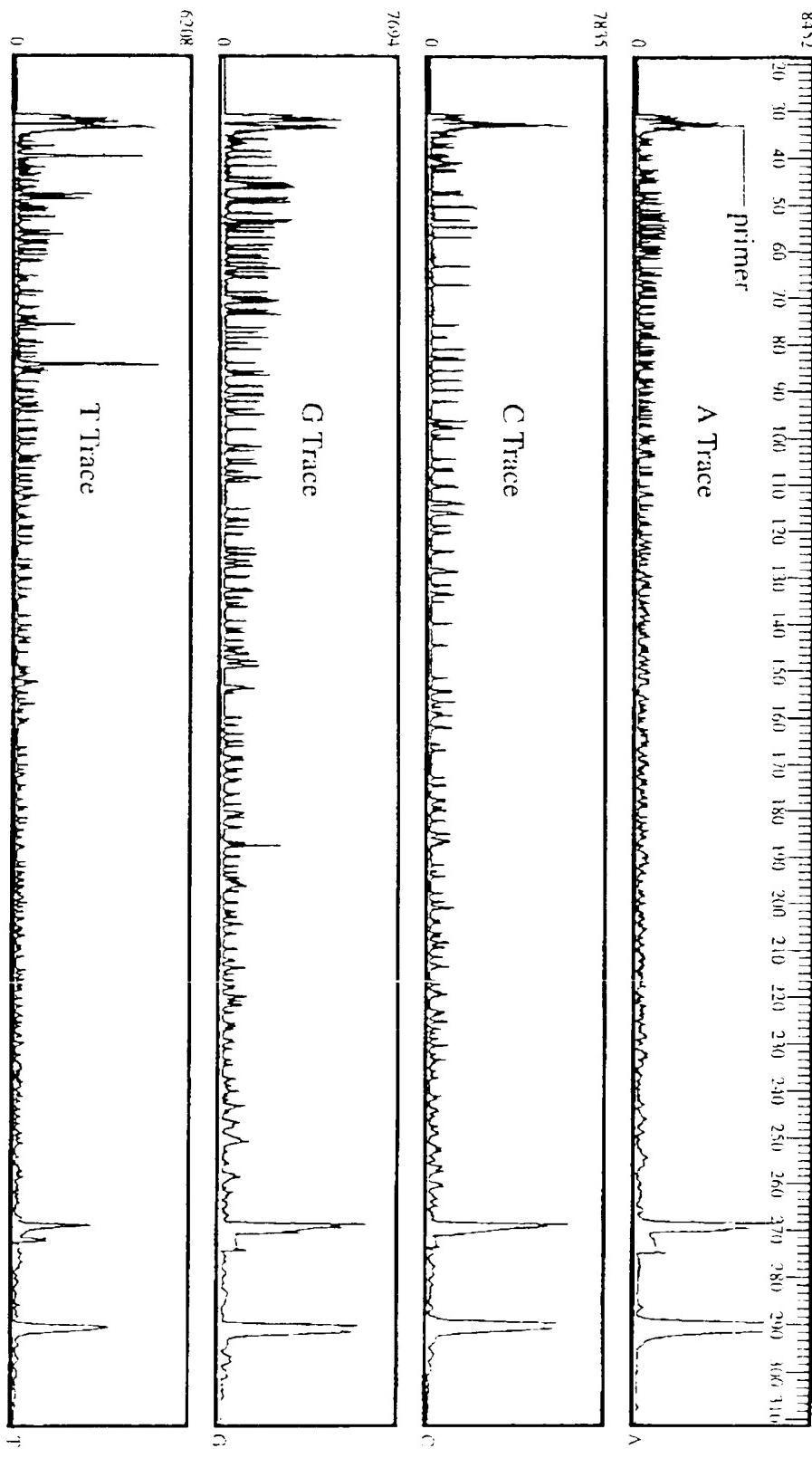
FIG. 9A

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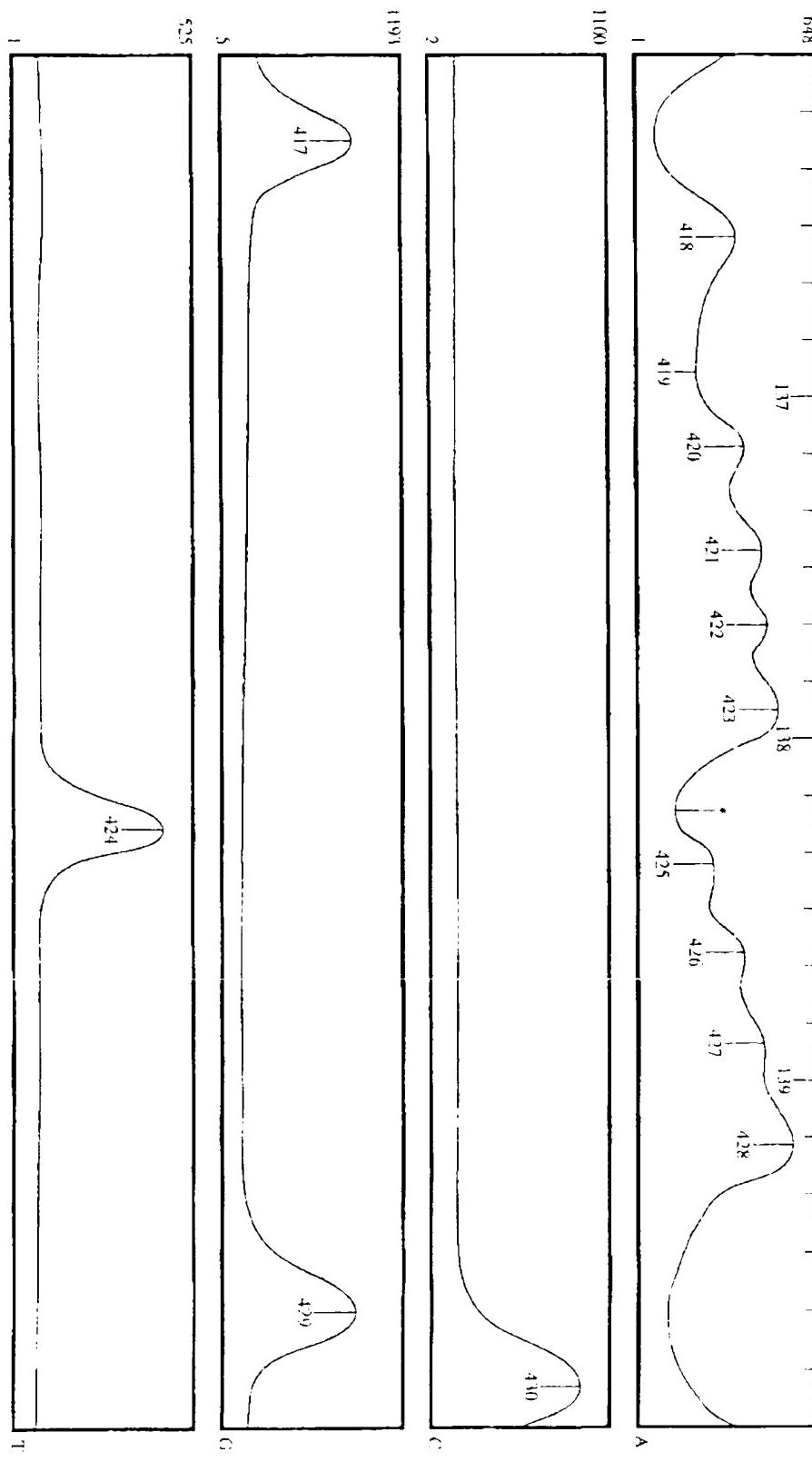
**FIG. 9B**
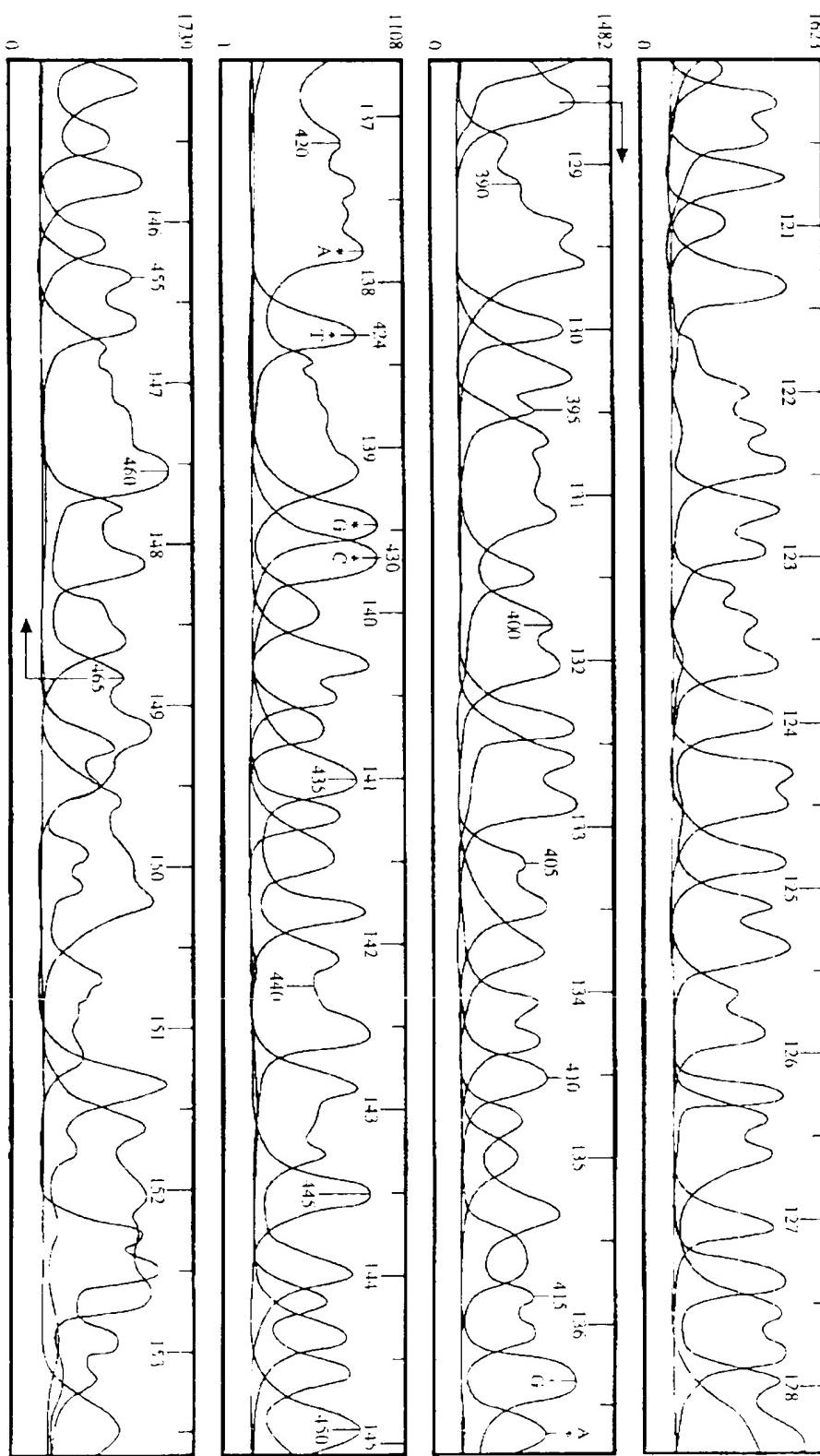
Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

FIG. 9C

Deviation of the Peak Position (in Number of Bases) from the Average as a Function of Base Number in Different Traces Before Alignment

FIG. 10
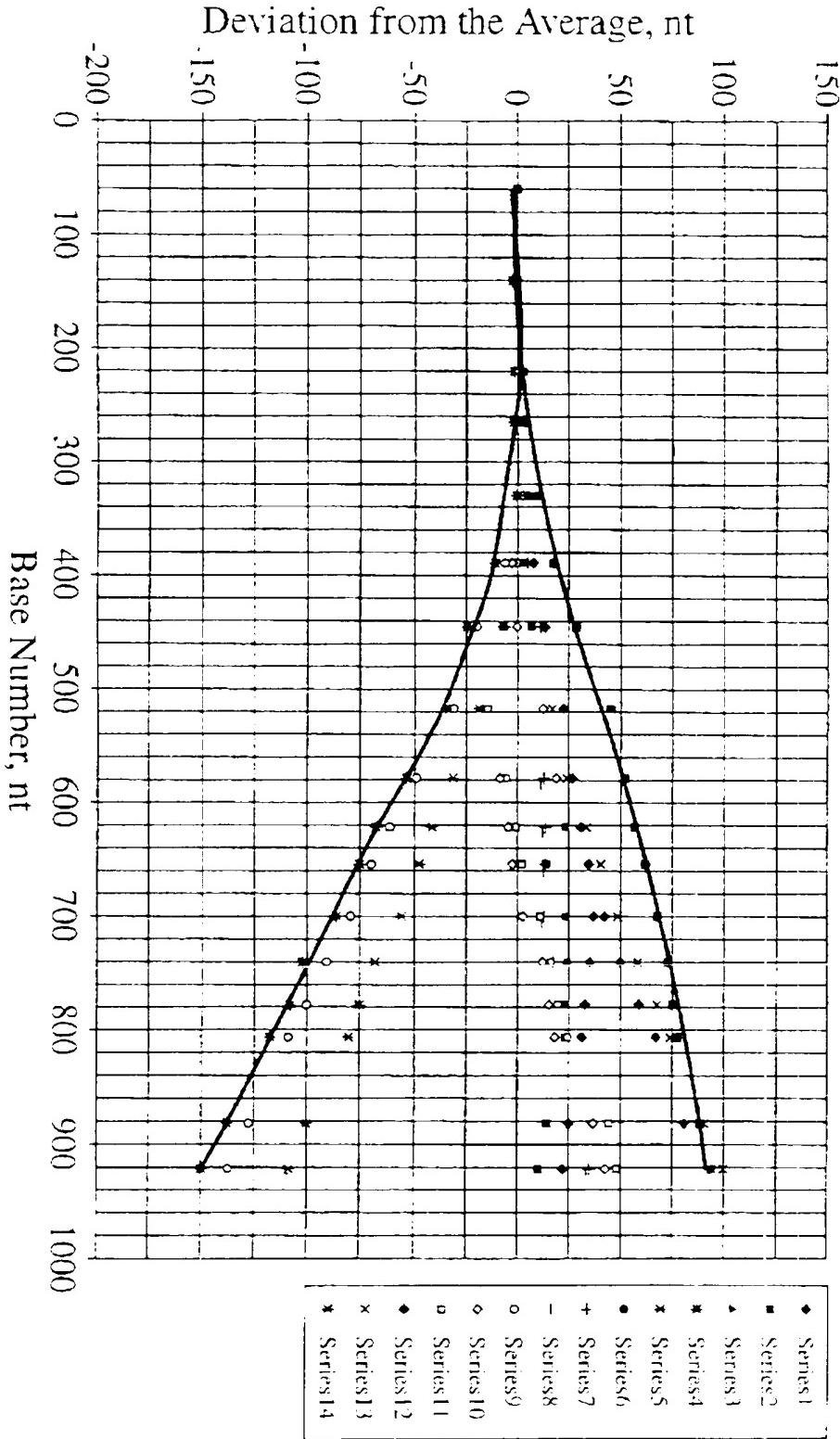
Legend:
- ◆ Series1
- ■ Series2
- ▲ Series3
- ✕ Series4
- ✳ Series5
- ● Series6
- + Series7
- − Series8
- ○ Series9
- ◇ Series10
- □ Series11
- ◆ Series12
- ✕ Series13
- ✳ Series14

**Deviation of the Peak Position (in Number of Bases) from the Average
as a Function of Base Number in the Traces Aligned with Internal Standards
(long gel, M13, 17 peaks, 5-th degree polynomial)**

FIG. 11

Series1
Series2
Series3
Series4
Series5
Series6
Series7
Series8
Series9
Series10
Series11
Series12
Series13
Series14